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# Reassessment of French breeding bird population sizes using citizen science and accounting for species detectability

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## **ABSTRACT**

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Large-scale and long-term biodiversity monitoring can be improved by the use of Essential Biodiversity Variables, among which species population sizes provide key data for conservation programs. Relevant estimations and assessment of actual population sizes are critical for species conservation, especially in the current context of global biodiversity erosion. However, knowledge on population size varies greatly, depending on species conservation status and ranges. While the most threatened or restricted-range species generally benefit from exhaustive counts and surveys, monitoring efficiently common and widespread species tends to be neglected or is simply more challenging to achieve. In such a context, citizen science (CS) is a powerful tool for the long-term monitoring of common species through the engagement of various volunteers, permitting data acquisition on the long term and over large spatial scales. Despite this substantially increased sampling effort, detectability issues imply that even common species may remain unnoticed at suitable sites. The use of structured CS schemes, including repeated visits, enables to model the detection process, permitting reliable inferences of population size estimates. Here, we relied on a large French structured CS scheme (EPOC-ODF) comprising 27 156 complete checklists over 3 873 sites collected during the 2021-2023 breeding seasons to estimate the population size of 63 common bird species using Hierarchical Distance Sampling (*HDS*). These population size estimates were compared to the previous expert-based French breeding bird atlas estimations, which did not account for detectability issues. Our results indicate strong under-estimations for 65% of species in the French atlas, likely due to more conservative estimates inferred from semi-quantitative expert-based assessments. We also found a few over-estimations for species with long-range songs such as *Cuculus canorus*, *Upupa epops* or *Turdus merula*. Our study highlights the need to rely on sound statistical methodology to ensure unbiased ecological inferences with adequate uncertainty estimation and advocates for a higher reliance on structured CS in support of biodiversity monitoring.

**Keywords:** Bird atlases ; Biogeography ; Breeding Bird Surveys ; Citizen Science ; Detectability ; Hierarchical Distance Sampling

Worldwide bird populations are nowadays caught in the midst of a global, man-driven erosion of biodiversity caused by the synergistic effects of habitat loss and fragmentation, resource overexploitation, climate change, pollution, pesticide use as well as the global spread of invasive species (Ceballos et al., 2015; Johnson et al., 2017; Rigal et al., 2023). Recent researches have pointed out how important species-specific life attributes (e.g., species range and density) and functional traits (e.g., body mass, diet or dispersal) explain long-term bird trends and responses to global changes (Germain et al., 2023; Gregory et al., 2023; Hong et al., 2023; Santini et al., 2023). Monitoring long-term as well as shorter-term trends have been historically possible through standardised biodiversity - including bird - surveys at a national scale and aggregated at the continental one (Brlík et al., 2021; Jiguet et al., 2012; Pilotto et al., 2020). This monitoring produces comprehensive distribution atlases pointing out current ranges and their historical changes (Keller et al., 2020), as well as long-term population trends (Brlík et al., 2021). Identifying common species declines should help guide agricultural and planning policies (Gaston and Fuller, 2008; Rigal et al., 2023), so as to reconcile societal needs with the need to safeguard biodiversity (Couvet and Ducarme, 2014).

Monitoring the success of the implementation of such policies is possible through the measurement of Essential Biodiversity Variables (Jetz et al., 2019; Navarro et al., 2017; Pereira et al., 2013), including the assessment of species distribution range and population abundance or density (Santini et al., 2023). Global monitoring capabilities of species populations have increased over the past few decades as citizen science (CS) has gained prominence across various domains, particularly in ecology (Kullenberg and Kasperowski, 2016). This participatory approach has provided the public with unprecedented opportunities to contribute to biodiversity monitoring through data collection and indirectly through their engagement in policy evaluation (McKinley et al., 2017).

The development of CS can be related to the emergence of multiple online databases (Newman et al., 2012) capable of gathering comprehensive datasets across large spatial scales and multiple taxa such as iNaturalist ([www.inaturalist.org](http://www.inaturalist.org)) and BioloVision ([data.bioloVision.net](http://data.bioloVision.net)) or taxa-centered, for instance, eBird ([www.ebird.org](http://www.ebird.org)). The emergence of CS databases has thus resulted in an exponential increase in biodiversity monitoring capabilities, ranging from phenological shifts (Hurlbert and Liang, 2012), species distribution (Matutini et al., 2021; Suzuki-Ohno et al., 2017) and abundance estimation (Callaghan et al., 2021).

Traditionally, species autecology was recensed in atlases providing temporal snapshots of known distribution and population size estimates using discontinuously gathered data collected during a short period (Donald and Fuller, 1998) and allowing long-term changes assessment when repeated over decades (Keller et al., 2020). The first attempt of French avifauna compilation dates back to 1936 (Mayaud et al., 1936) while the first national atlas was published in 1976 (Yeatman et al., 1976) followed by subsequent in 1995 (Yeatman-Berthelot and Jarry, 1995) and 2015 (Issa and Muller, 2015). Each

91 iteration was marked by a significant increase in participating citizen birders, ranging from 500 to 2400  
92 then to 10,000. However, while the ultimate aim of bird atlases is to acquire even knowledge across  
93 multiple species for a given geographical area (typically national-wide inquiries), it is essential to note  
94 that rare and threatened species benefit from more in-depth population monitoring than more frequent  
95 and abundant ones (Ingram et al., 2021). Such exhaustive knowledge of rare species populations is due to  
96 interest risen by high extinction risk (IUCN, 2001), the need for recovery plans (Farrier et al., 2007) and  
97 narrow distributions allowing exhaustive counts (Quaintenne et al., 2020). In contrast, common species  
98 (being altogether abundant and widespread (Rabinowitz, 1981)) considered Least Concern (LC) tend to be  
99 neglected or simply overlooked (Neeson et al., 2018) despite being key components of global avian  
100 biomass changes (Gaston and Fuller, 2008; Inger et al., 2015; Rigal et al., 2023; Whelan et al., 2015).

101 The principal cause of low quantitative coverage of common birds can be tied to the lack of specific  
102 funding stemming from a conservation prioritisation approach (Brooks et al., 2006; Meine et al., 2006)  
103 and the trade-off between data quality and data acquisition over large spatial scales (Devictor et al.,  
104 2010; Kamp et al., 2016). In France, this incomplete knowledge translates into a significant drop in quality  
105 for population size estimates of most common bird species, where 60% of breeding species population  
106 estimates are qualified as medium while for rare and localised species (24% of species), estimates are  
107 considered as highly reliable (Comolet-Tirman et al., 2022). To account for this discrepancy, a semi-  
108 quantitative estimation method was used for the last atlas survey, with population sizes simply inferred  
109 from the average number of breeding pairs measured over 10x10km grid cells using abundance classes of  
110 1-9, 10-99, 100-999, 1000-6666 (the last upper limit could vary according to knowledge about species  
111 densities) multiplied by the number of grid cells known for nesting. Population sizes estimated using this  
112 method correspond to lower and upper limits. Lower limits were obtained by calculating the arithmetic  
113 mean of the abundance classes weighted by the number of 10x10 grid cells belonging to these  
114 abundance classes while upper limits were obtained by using the geometric means (see Roché et al.,  
115 2013 method referred further as *ArGeom*).

116 However, similarly to other studies (Kellner and Swihart, 2014), this approach fails to account for  
117 species detectability  $p$  defined as the probability of detecting at least one individual of a given species in  
118 a particular sampling effort, given that individuals of that species are present in the area of interest  
119 during the sampling session (Boulinier et al., 1998). Numerous studies have previously shown that  $p$   
120 varies with time of day and season (Skirvin, 1981), observers (Quinn et al., 2011) and year-specific factors  
121 (Kéry and Schmid, 2004). Omitting species detectability by assuming perfect or constant  $p$  across  
122 sampling schemes, observers and habitat types can lead to biased inferences (Kéry, 2011; Nichols et al.,  
123 2009) and affect the estimation of long-term trends due to its unaddressed variation (Sanz-Pérez et al.,  
124 2020; Schmidt et al., 2013). Hence, building on the joint effort in (i) standardisation of data acquisition to  
125 enhance the quality of inferences derived from raw species abundance data, following similar path as the  
126 FBBS (French Breeding Bird Survey) did for trend monitoring (Jiguet et al., 2012); and (ii) the development

127 of a workflow that uses statistical models accounting for the detection process, we propose an  
128 estimation method enabling a more robust approach of population sizes with associated uncertainty  
129 intervals.

130 In this study, we aimed at (i) testing whether an unprecedented large citizen-based dataset collected  
131 over France would provide a new, closer-to-truth quantitative evaluation of French breeding bird  
132 populations and at (ii) comparing population sizes inferred through Hierarchical Distance sampling from  
133 those inferred using the previous atlas methodology *ArGeom* for a significant part of French avifauna. In  
134 particular, we expect that quantifying the influence of species detectability would allow more relevant  
135 ecological inferences (e.g., including environmental and effort covariates to the models) to approach  
136 closer to a realistic estimation of breeding bird population size at a national level than previously used  
137 methodologies.

138

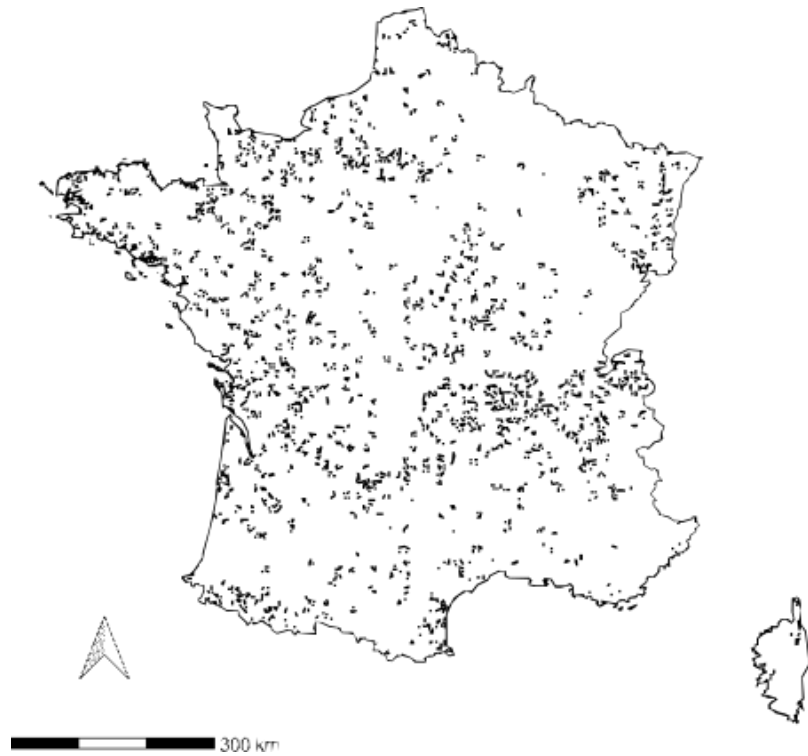
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## Materials and methods

### 140 Sampling protocol

141 EPOC-ODF (French structured estimation of breeding bird population size) is a French CS monitoring  
142 scheme based upon 5-minute point counts, where observers are tasked to point precisely encountered  
143 individual bird locations. Birders can register their field observations directly using the NaturaList  
144 smartphone application or transcript later on the data portal Faune-France ([www.faune-france.org](http://www.faune-france.org)).  
145 Survey locations are randomly selected from a systematic grid and have to be visited three times during  
146 the breeding season, from march to june , each consisting of three successive 5-minute point counts  
147 considered as temporal replicates, see Appendix S1 for more details.

148 Over the 2021 and 2023 breeding seasons, 276 distinct species were encountered over 27 156  
149 complete checklists collected over 3 873 pre-selected locations (Fig 1) by 520 observers. Sampling effort  
150 is monitored through local associations tasked to recruit volunteers. The primary focus of the scheme  
151 being the monitoring of common breeding bird species, we decided to constrain the number of species  
152 considered viable targets of this scheme to 103 out of the 276 species contacted.



153

154 **Figure 1** - Spatial distribution of surveyed EPOC-ODF locations (n = 3 505) over 2021-2023 breeding  
 155 seasons.

156 **Bird species selection and environmental covariates**

157 We narrowed our study to 63 species out of the initial set of 103, comprising only those recorded at a  
 158 minimum of 150 distinct locations (3.9% of locations), to have enough data to reach model convergence.  
 159 We also applied a temporal filter that considered both observed activity during the breeding season and  
 160 expert opinion to capture the breeding phenology of each targeted species and exclude possible early or  
 161 late migrants from population size estimates (see Appendix S2.1).

162 For bioclimatic data, we used 19 variables from WorldClim at 1km resolution (Fick and Hijmans,  
 163 2017), on which we applied a Principal Component Analysis (PCA), keeping the first three axes (82.3% of  
 164 explained variance), in order to limit multicollinearity through orthogonal transformation (Cruz-Cárdenas  
 165 et al., 2014).

166 We used habitat cover data from Theia OSO at 10m resolution (Thierion et al., 2022) and aggregated  
 167 it according to two different scales: (1) a seven-class corresponding to habitat type (Urban, Annual crops,  
 168 Perennial crops, Pastures, Grasslands, Forests, Water body/Mineral surfaces) and (2) three-class (Open,  
 169 Forests, and Artificial) in regards to overall effect on detectability (Appendix S3). Additionally, we  
 170 conducted PCA dimension reduction on the seven-class aggregation, retaining three of the six PCA  
 171 (54.71% of explained variance) axes for ease of comprehension and examination; see Appendix S3 for the  
 172 workflow pipeline and habitat cover aggregation. Distances to roads were measured from ROUTE 500®  
 173 (Cote et al., 2021).

174 Bioclimatic variables and seven-class habitat covers were collected over 500m buffer radii upon the  
175 registered observer location as landscape variable. These distances were chosen according to mean  
176 dispersal distances and home range sizes in common European birds (Paradis et al., 1998). The three-  
177 class habitat covers were collected upon 100m circles radii to assess immediate habitat type that could  
178 hinder species detection. Whenever the exact location was unavailable, we used the centroid of sightings  
179 as a proxy for observer location (Appendix S4).

180 We used environmental data collected from a prediction grid covering France at a resolution of  
181 2x2km for PCA dimension reduction. Outcomes from this initial PCA were used to transform  
182 environmental data collected from surveyed locations through PCA projections.

183

## 184 **Modelling approach**

185 We used Hierarchical Distance Sampling (*HDS*) models to estimate the abundance of the target  
186 species while accounting for uncertainty arising from the observation process (Chandler et al., 2011; Kéry  
187 and Royle, 2015). We applied a right-side truncation of 5% over the observation distance for each  
188 targeted species to remove extreme distance values for model robustness (Buckland et al., 2001). Then,  
189 we divided observation distances into five proportional bin classes based on the maximal observed  
190 distance. Models calibration and assessment were done using *unmarked* 1.2.5 R package (Fiske and  
191 Chandler, 2011). Effort covariates were accounted for by incorporating the Julian date and the hours of  
192 list realisation (as minutes from sunrise).

193 Distance sampling key functions, depicting detection probabilities fall-off given distance of  
194 observation (Buckland et al., 2001), were chosen between half-normal and hazard-rate based on AIC  
195 (Akaike Information Criterion, Akaike, 1974), with other states kept constant.

196 We based our modelling framework on a secondary candidate set strategy, where the detection and  
197 availability states of our *HDS* were fit according to the set of the first candidates while others were kept  
198 constant (Morin et al., 2020). For the Poisson process underlying abundance distribution, we used a  
199 single model consisting of retained covariate PCAs axes.

200 *HDS* population size estimates were obtained through averaging retained secondary candidate sets  
201 models, based on their relative model performance using AICc, except for the Eurasian Sparrowhawk  
202 (*Accipiter nisus*), the Meadow Pipit (*Anthus pratensis*) and the Coal tit (*Periparus ater*), we exclusively  
203 employed prediction from best final models owing to substantial differences observed among their  
204 secondary candidate sets models.

205 All models were fit according to a Poisson (P) distribution after top model assessment and calculation  
206 of overdispersion coefficient ( $\hat{C}$ ), secondary candidate sets with  $\hat{C}$  top models exceeding 1.2 were  
207 calibrated using a Negative binomial (NB) distribution (Payne et al., 2018). For a global overview of our  
208 modelling approach, see Appendix S5.



209 Out of 63 species, we excluded nine species from the analysis; three exhibited signs of  
210 underdispersion with  $\hat{C}$  values less than 0.9 while six had  $\hat{C}$  value exceeding 1.5 (Payne et al., 2018),  
211 showing signs of overdispersion, despite being calibrated using a negative binomial distribution, see table  
212 S2.1 for more details.

213 We assessed the robustness of our estimations by comparing population size estimates calibrated  
214 using all available data from 2021 to 2023, with a subset of data collected from 2021 to 2022. Using the  
215 2021-2022 subset, we estimated the population sizes of 30 species, detected in at least 150 distinct sites.

216 From these 30 species, nine mean population sizes estimated using 2021 to 2023 data were outside  
217 the confidence intervals estimated from 2021 to 2022 data, with slightly smaller population size  
218 estimated (Table S2.2) overall highlighting robust estimations.

219

## 220 **Population estimation and extrapolation assessment**

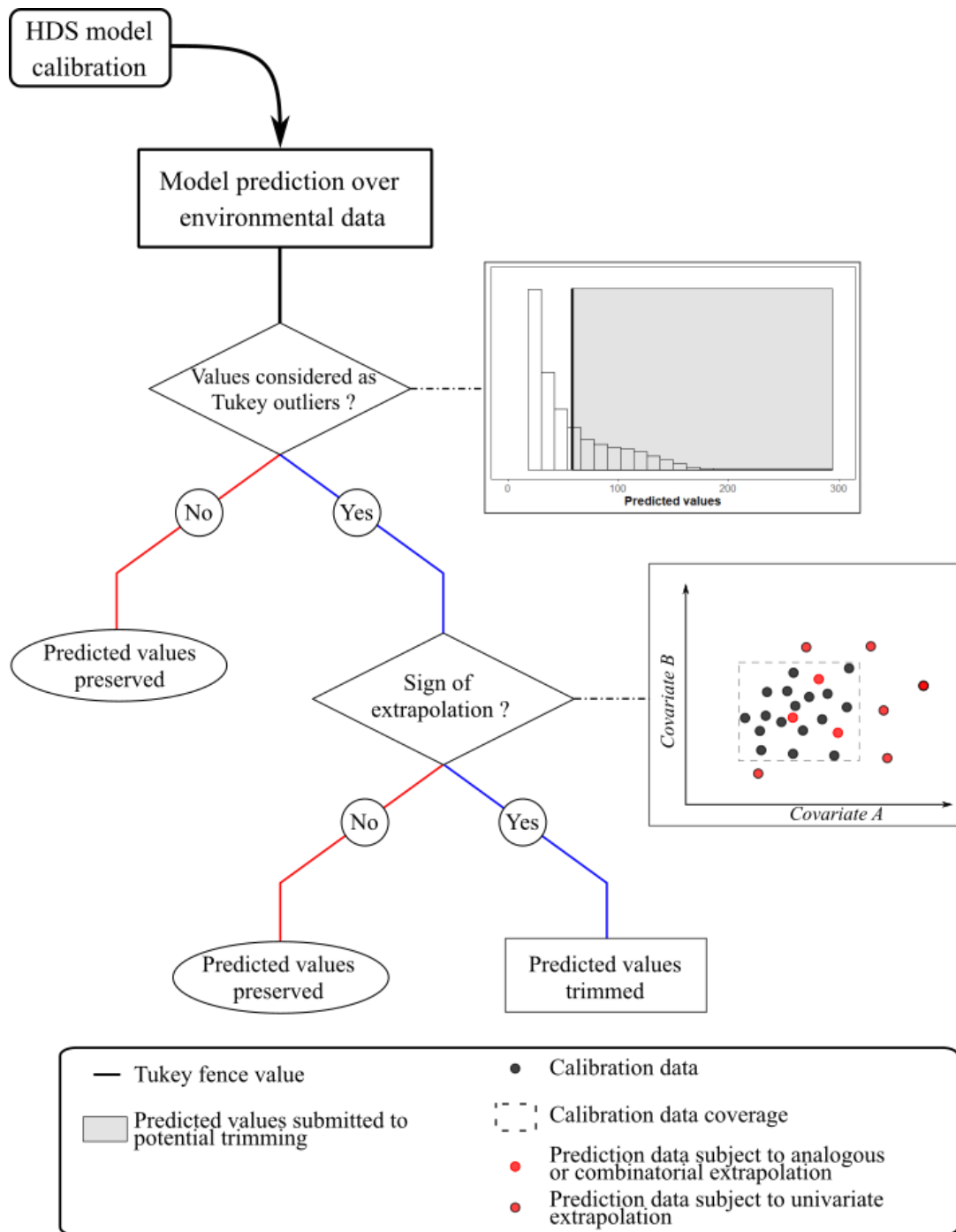
221 Population sizes were obtained by summing predicted values over the prediction grid. As we intend  
222 to predict over a large surface, novel environmental conditions may arise, leading to possible  
223 dissimilarities between the environmental gradient collected at survey sites and the environmental  
224 gradient over novel conditions (Elith and Leathwick, 2009).

225 Mesgaran et al., 2014 described two types of extrapolation ; (i) Novelty type I (NT1) where projected  
226 points (i.e prediction grid) are outside the range of individual covariates collected by the sampling  
227 scheme and (ii) Novelty type II (NT2) depicting the case when projected points are within univariate  
228 range but constitute novel combinations between covariates.

229 We trimmed predicted values (Fig 2.) over prediction grid cells showing signs of NT1 extrapolation, to  
230 a threshold value determined using a Tukey fence (Tukey, 1977), estimated from the distribution of  
231 predicted values with  $k=1.5$ . Extrapolation assessment were done using *dsmextra* 1.1.5 R package  
232 (Bouchet et al., 2020).

233 We used this post-prediction treatment to assess population size estimates stability by measuring the  
234 coefficient of variation of the range uncertainty between pre- and post-treatment estimates.

235 Large coefficient of variation implies great discrepancies between confidence intervals between pre-  
236 and post-treatment. This is mainly caused by the spatial filtering from the extrapolation assessment  
237 highlighting smaller geographic regions with similar environmental conditions from sampled ones and the  
238 trimming of predicted abundance outliers. Species with a coefficient of variation exceeding 30% were  
239 removed from the comparison analysis (Table S2.3).



240

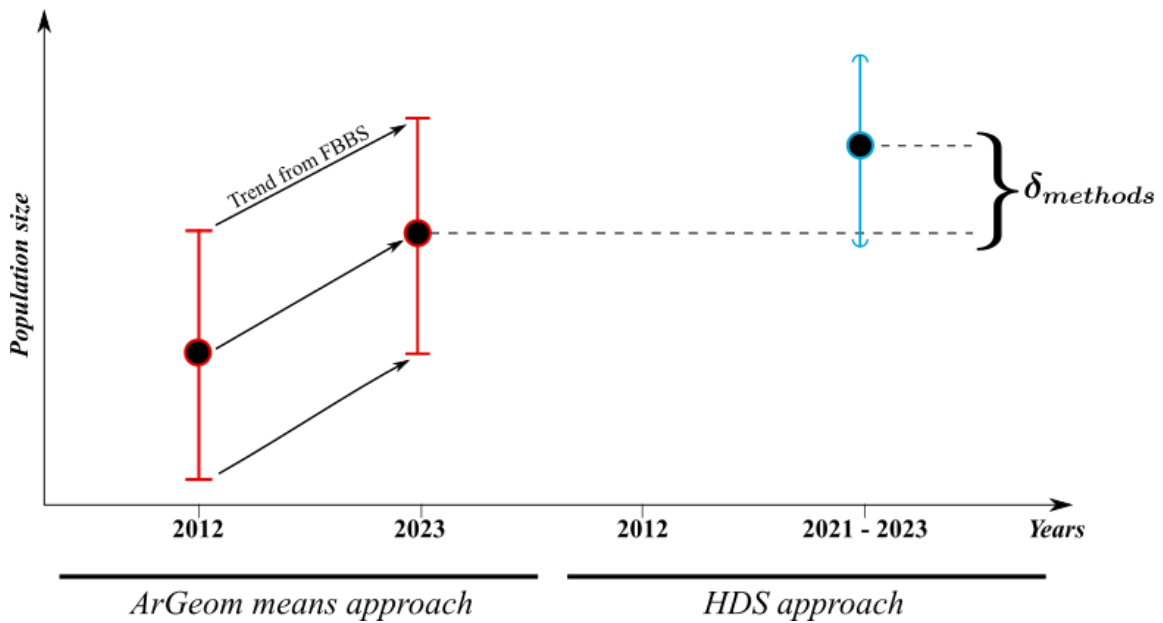
241 Figure 2 - Decision tree of the post-prediction treatment. First, we analysed the distribution of predicted  
 242 abundance values across the prediction grid and detected outliers, using a hinge of  $k = 1.5$  (Tukey, 1977).  
 243 We compared each environmental condition of the prediction grid cell with the environmental condition  
 244 collected by the sampling scheme and used for model calibration. When a prediction cell depicted signs  
 245 of NT1 extrapolation and its estimated abundance was considered as an outlier, we trimmed the  
 246 predicted grid cell abundance to the Tukey fences value.

247

248 **Estimates comparison**

249 In order to have comparable estimates, we restricted the prediction grid area species-wise for *HDS*  
 250 estimation according to the distribution of their known breeding locations, collected over a 10x10km grid  
 251 during the previous French atlas (Issa and Muller, 2015). To estimate breeding populations of species for  
 252 which male identification was possible, either male vocalisations or visual distinctions because of sexual  
 253 dimorphism, an ad-hoc filter was applied (Table S2.1), resulting in *HDS* estimates reflecting the male  
 254 counts for those species. For species where male identification in the field was impossible (no sexual  
 255 dimorphism), we used all available data after applying the phenological filter and divided *HDS* estimates  
 256 by two for comparison with *ArGeom* estimates.

257 *ArGeom* population size estimates were retrieved from the previous French atlas (Issa and Muller,  
 258 2015; Roché et al., 2013), and combined with recent population trend estimates derived from French  
 259 breeding bird survey (FBBS) data spanning 2012-2023 (Table S2.1). Given the absence of a mean estimate  
 260 in the *ArGeom* approach, we approximated it using the midpoint between the maximum and minimum  
 261 estimated (Fig 3.).



262

263 **Figure 3** - Population size estimates comparison methodology, *ArGeom* in red and *HDS* in blue. *ArGeom*  
 264 estimates for 2012 were obtained through calculations using both arithmetic and geometric means  
 265 (Roché et al., 2013) and were then updated to 2023 using specific mean trend estimates from FBBS  
 266 (Table S2.1). Flat intervals signify min/max value estimates, while curved intervals signify confidence  
 267 intervals.

268 To study the differences between the two approaches, we measured  $\delta_{methods}$  corresponding to the  
 269 percentage of the difference between *HDS* and *ArGeom* estimates.

270

$$\delta_{methods} = \frac{(Estimates_{ArGeom} - Estimates_{HDS})}{(Estimates_{ArGeom} + Estimates_{HDS})/2}$$

271

272 We also took account of *ArGeom* uncertainty corresponding to the difference between the maximal  
273 and minimal estimated values; population size variations across species were accommodated using  
274 decimal logarithm.

275

## 276 **Phylogenetic model**

277

278 As species detectability stems from physical traits and vocalisations, phylogenetic related species  
279 tend to have the same detectability (Sólymos et al., 2018). We calibrated a Phylogenetic Generalised  
280 Linear Mixed Models (PGLMM) using the phyloglmm 1.0 (Li and Bolker, 2019) R package, in order to  
281 study  $\delta_{methods}$  variations across species while taking account of species phylogenetic relatedness  
282 (Johnston et al., 2014; Sólymos et al., 2018). Phylogenetic distances were retrieved from Burleigh et al.  
283 (2015). The PGLMM model was calibrated using (i) retrieved detection probabilities from the availability  
284 state estimated through *HDS* (see Appendix S5), using weighted means final candidate sets models in  
285 regards to AICc scores, and (ii) *ArGeom* uncertainty as fixed variables. Response weights consisted of  
286 normalised weights from the inverse of uncertainty around FBBS trends between 2012 and 2023 (Table  
287 S2.1), divided by the mean in order to limit excessive weight attribution and facilitate model  
288 convergence.

289

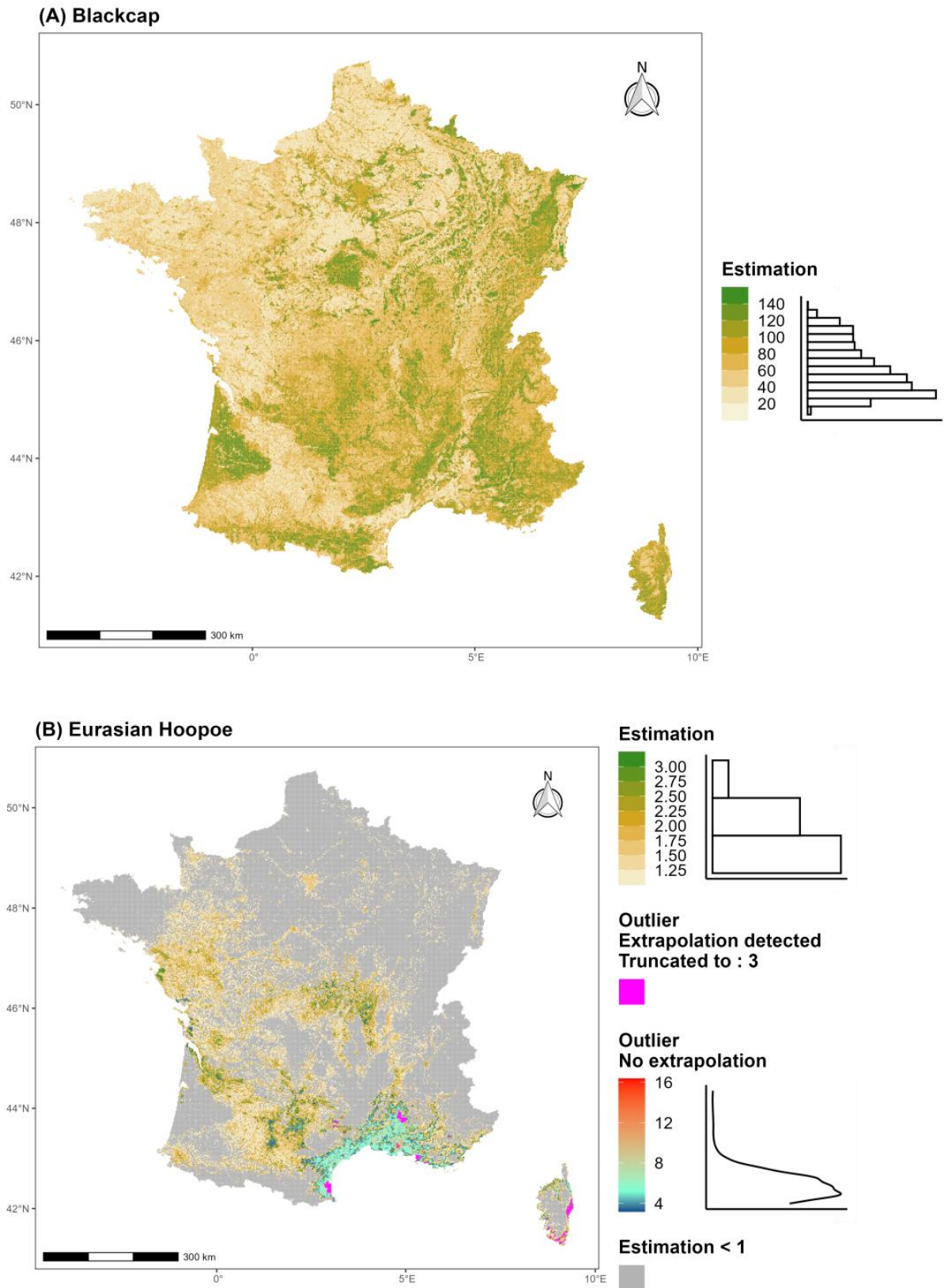
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## **Results**

291 From 2012 to 2023, out of 63 bird species, 15 showed a significant decrease ( $x = -22.79\% \pm 14.84$ ) in  
292 total population size, while 16 showed a significant increase ( $x = 28.02\% \pm 22.52$ ; see appendix S2 for  
293 species-related FBBS trends).

294 Out of the 54 species with acceptable values of overdispersion ( $\hat{C}$ ) using the *HDS* approach, we  
295 excluded eight species showing large discrepancies in population size estimates (Appendix S2, Table S2.3)  
296 between pre- and post-prediction treatment (Fig. 2.).

297 Out of the remaining 46 species used for comparison between *ArGeom* and *HDS* estimates, *HDS*  
298 models showed acceptable values of overdispersion ( $\hat{C}$ ) ranging from 0.94 to 1.2 ( $x = 1.07 \pm 0.06$ ) for 38  
299 species calibrated using a Poisson distribution and 1.09 to 1.47 ( $x = 1.27 \pm 0.13$ ) for eight species  
300 calibrated using a Negative binomial distribution. Across all species, estimated mean density ranges from  
301 0.09 to 27.51 individuals per square kilometre, while *ArGeom* range uncertainty varied from 3.9 to 6.69  
302 on the decimal logarithm scale corresponding to variations from 7,920 to 4,850,000 in estimated number  
303 of pairs (Table S6.1-2).



304

305 **Figure 4** - Examples of resulting abundance maps for the (A) Blackcap *Sylvia atricapilla*, and (B) Eurasian  
 306 Hoopoe *Upupa epops*. Estimations correspond to the number of male, or potential pairs (see Table S2.3)  
 307 over a 4 km-squared area. Grid cell predictions are categorised into three groups: (1) those with

308 estimated abundance not considered as outliers depicted with a green colour step gradient and sits  
309 distribution histogram ; (2) those with estimated abundance considered as outliers and showing no  
310 extrapolation signs, displayed in a blue-to-red gradient, along with their distribution density ; and (3)  
311 those with estimated abundance considered as outliers with novel environmental conditions subject to  
312 NT1 extrapolation highlighted in pink with the tukey value used for trimming in the post-prediction  
313 treatment.

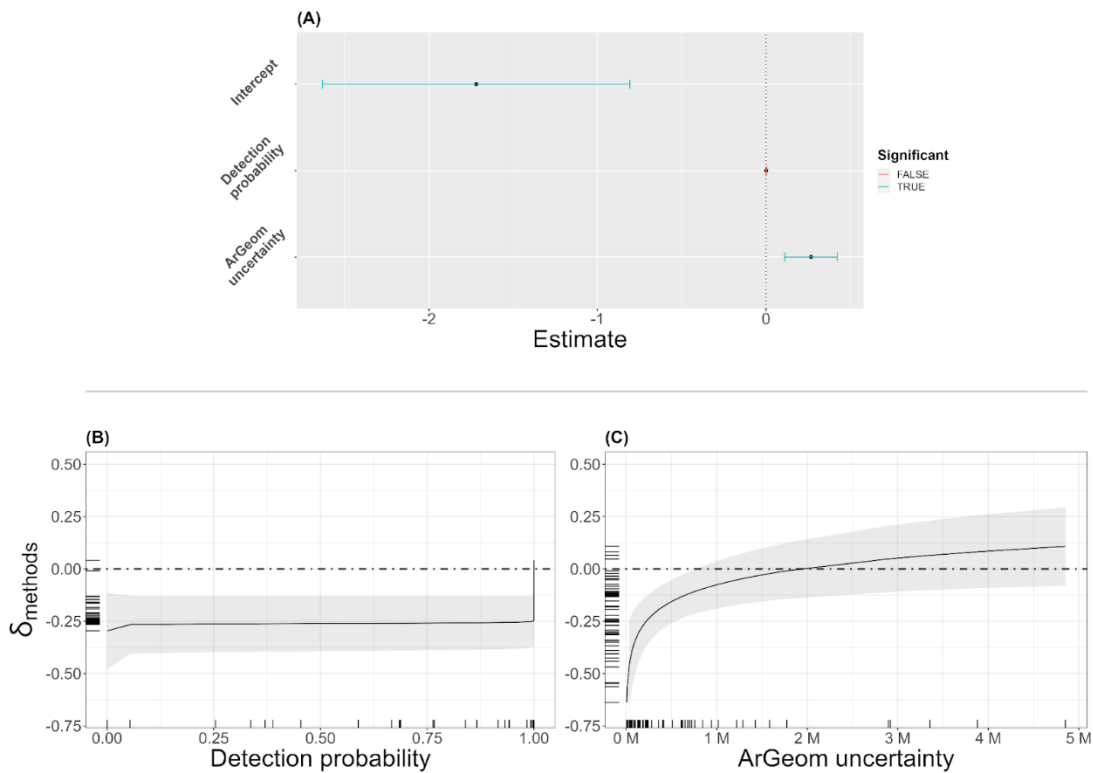
314

315 A comparison between updated *ArGeom* and *HDS* estimated population sizes showed that *HDS*  
316 estimates were higher than *ArGeom* for 30 of the 46 species tested (Table S6.1). Our results suggest a  
317 larger under-estimation of *ArGeom* ( $\delta_{methods} < -0.2$ ) estimates for either habitat specialist species such  
318 as Stonechat (*Saxicola rubicola*), European Goldfinch (*Carduelis carduelis*), Eurasian Linnet (*Carduelis*  
319 *cannabina*) or Great spotted woodpecker (*Dendrocopos major*) and some generalist species such as Blue  
320 tit (*Cyanistes caeruleus*) or Blackcap (Fig 4.A) with  $\delta_{methods} = -0.629 \pm 0.4$ , over 22 species. Species  
321 whose estimations were similar ( $\delta_{methods} \in [-0.2;0.2]$ , with on average  $\delta_{methods} = -0.006 \pm 0.096$ , over  
322 17 species) between *ArGeom* and *HDS* included species such as Eurasian Wren (*Troglodytes troglodytes*),  
323 Great tit (*Parus major*), European Robin (*Erithacus rubecula*) and European Nuthatch (*Sitta europea*).  
324 Fewer species, mainly characterised by greater maximal observation distances, such as Common cuckoo  
325 (*Cuculus canorus*), Eurasian hoopoe (Fig 4.B) and European Blackbird (*Turdus merula*) had their  
326 population size estimates overestimated by *ArGeom* approach compared to *HDS* ( $\delta_{methods} > 0.2$ , with on  
327 average  $\delta_{methods} = 0.41 \pm 0.148$ , over 7 species ; see Appendix S6 for population size comparison table).

328 Results from the PGLMM (Fig 5.A) showed an overall significant under-estimation of *ArGeom*  
329 estimates (-1.625, with 95% CI : [-2.553;-0.699], P = 0.001), as well as a significant positive effect of  
330 *ArGeom* range intervals (0.248, with 95% CI : [0.087;0.409], P = 0.003) on the differences between the  
331 two approaches. Species detection probabilities had no significant effect (0.003, with 95% CI : [-  
332 0.001;0.007], P = 0.176) on  $\delta_{methods}$  variation.

333 Marginal effect plots from the PGLMM model showed that the mean response of  $\delta_{methods}$  over  
334 species detection probability was predominantly negative, ranging from -0.45 to -0.1 (Fig 5.B), for  
335 *ArGeom* uncertainty. This showed that  $\delta_{methods}$  tended towards the convergence of population size  
336 estimates (Fig 5.C) for species with larger estimated interval ranges. There were no signs of  
337 multicollinearity (VIF < 5 ; James et al., 2013) between the two variables.

338



339

340 **Figure 5** - Results from the PGLMM. (A) Confidence intervals of the model coefficient, parameters,  
 341 coefficients significantly different from 0 are represented in blue. Marginal effect plots of population size  
 342 estimates differences ( $\delta_{methods}$ ) responses over species detection probabilities (B), and *ArGeom* reported  
 343 uncertainties in numbers of breeding pairs (C).  $\delta_{methods}$  responses are represented on variable natural  
 344 scales, after inverse logit and inverse decimal logarithm transformation, respectively. Dot-dash line  
 345 corresponds to a  $\delta_{methods}$  of 0, signifying estimated population sizes convergence by the two  
 346 approaches, negative and positive values of  $\delta_{methods}$  reflect under and over-estimation of *ArGeom*  
 347 population size estimate relative to *HDS*.

348

349

## Discussion

350 Our results showed an overall under-estimation of former population sizes for 65% of bird species  
 351 estimated for the French national territory (i.e., from *ArGeom* estimates) without explicitly accounting for  
 352 species detectability. While we found that the presumed known uncertainties ranges had a positive  
 353 effect on the convergence of population sizes estimated by the two methodological approaches (expert  
 354 estimates based on atlas data vs predicted estimates from modelled citizen science data accounting for  
 355 detection probabilities), we did not find a significant effect of species detection probabilities which could  
 356 explain the differences between the two approaches. Major under-estimation in population sizes ( $\delta <$   
 357 0.2) seems to affect species regardless of habitat specialisation or habitat type and pointed out the  
 358 importance of the detection process in population size inferences.

359 Despite the lack of significant evidence for the effect of species detection probabilities on population  
 360 sizes estimations, our results tend to corroborate previous studies where ignored detection processes

361 may have biased ecological inferences, including species distribution models (Kéry et al., 2010),  
362 population trends (Norvell et al., 2003; Schmidt et al., 2013) and population sizes (Kéry et al., 2005). This  
363 may be especially true in a context of global change, where avian breeding phenology showed evidence  
364 of shifts towards earlier breeding over the years (Devictor et al., 2012; Gaüzère and Devictor, 2021;  
365 Parmesan, 2007) in order to synchronise with their food sources (Michel et al., 2016; Visser et al., 2006).  
366 Such shifts induce diverse species-related seasonal and inter-annual changes in detectability that need to  
367 be accounted for, particularly for schemes spanning over multiple species (Lehikoinen, 2013).

368 In France, the *ArGeom* approach was developed in the context of moderate quantitative data  
369 collection with a primary aim at giving likely population size estimates deviating from expert opinion  
370 reliance (Roché et al., 2013). As such, *ArGeom* intervals were estimated by extrapolation from a set of  
371 grid cells subject to estimations on all metropolitan grid cells considered suitable for breeding after the  
372 detection of probable and confirmed breeding evidence. Although proved useful and relevant to assess  
373 population sizes when large-scale quantitative data on species occurrences are lacking or are unevenly  
374 distributed, such a methodology implies greater uncertainty intervals for abundant and broad  
375 distribution species and smaller intervals for scarce and narrow distribution species when not accounting  
376 for measurement uncertainty.

377 Contrary to generalist species, which are widespread due to broader ecological niche breadths,  
378 specialists are generally more localised (Clavel et al., 2011) and use a lower range of habitats (Julliard et  
379 al., 2006). Despite a growing interest in rare species-focused monitoring (Fontaine et al., 2022), citizen  
380 science programs are mainly designed for large-scale multi-species surveys (Devictor et al., 2010) which  
381 sampling scheme, either structured or unstructured, could lead to habitat misrepresentation of localised  
382 species (Buckland and Johnston, 2017). Such misrepresentation translates to less acquisition of relevant  
383 information and could hinder ecological inferences about such species (Gaston et al., 1997; Mackenzie et  
384 al., 2005).

385 A recent study about long-term effects of climate and land use changes on bird communities  
386 (Gaüzère et al., 2020) showed that both generalist cold-dwelling species, such as the Common Chiffchaff  
387 (*Phylloscopus collybita*) or the Eurasian Blackcap, and warm-dwelling species, such as the common  
388 Nightingale (*Luscinia megarhynchos*) had the most substantial negative and positive contributions to the  
389 trend in Community Thermal Index (CTI), a community-weighted index representing the realised thermal  
390 niche of a community based upon species relative abundance and species thermal indices (STIs). In the  
391 present study, these species tended to be under-estimated when the detection process was omitted  
392 compared to estimates based on our modelling approach. As a result, this could lower the estimations of  
393 their contribution to the calculation of community-weighted mean indices, such as CTI, and therefore  
394 bias the estimation of the trend in community thermal response and subsequent studies of aggregated  
395 indices, which are known to display large regional variation (Rigal and Knape, 2024). We therefore



396 suggest that considering the detection process in studies relying on community-weighted indexes by  
397 species' relative abundances could be as important as it is for estimating population sizes.

398 Actually community indices, such as species diversity (Ricotta, 2005) and functional diversity (Gauzère  
399 et al., 2019; Villéger et al., 2008) are commonly using species relative abundance as a basis, without  
400 taking into account the detection process (Pillar and Duarte, 2010), despite multiple studies showing it  
401 could affect community indices inference (Jarzyna and Jetz, 2016; McNew and Handel, 2015; Richter et  
402 al., 2021; Tingley and Beissinger, 2013).

403 Our study also suggested that under- or over-estimation of population sizes were not randomly  
404 distributed among species according to their conservation status. Out of the 46 species estimation used  
405 in the comparison analysis, 10 had an unfavourable conservation status in France (i.e. lower than Least  
406 Concern, LC ; UICN France et al., 2016).

407 Among these species of conservation concern, while two species, European Greenfinch (*Carduelis*  
408 *chloris*) and European Turtle-Dove (*Streptoptelia turtur*), showed no signs of under-estimations ; five  
409 species, including European Stonechat, Barn Swallow (*Hirundo rustica*), Red-backed Shrike (*Lanius*  
410 *collurio*), Eurasian Kestrel (*Falco tinnunculus*) and Willow warbler (*Phylloscopus trochillus*) considered as  
411 NT (Near Threatened) and three species, including Eurasian Linnet, European Goldfinch and European  
412 Serin (*Serinus serinus*) considered as VU (Vulnerable) showed large signs of under-estimation with the  
413 *ArGeom* approach (NT :  $\delta_{methods} = -0.608 \pm 0.217$  and VU :  $\delta_{methods} = -0.667 \pm 0.146$ ), potentially  
414 leading to smaller estimated population sizes using the *ArGeom* approach than their modelled ones. Our  
415 results showed that these species may need a reevaluation of their conservation status and highlights the  
416 need to rely on hierarchical models taking account of the detection process in ecological inferences given  
417 that potential misclassification of population conservation status comes from process noise and  
418 observation error (Connors et al., 2014).

419 Nevertheless, our approach has some drawbacks. It relies on data collected from the EPOC-ODF  
420 structured CS schemes, providing data with repeated visits. However, as is, the frequentist framework of  
421 *unmarked* R package does not permit inferences of clustered individuals (Fiske and Chandler, 2011).  
422 Taking account of social species during breeding season (corresponding to 1/10th of the scheme targeted  
423 species) would require a Bayesian framework (Clement et al., 2017). This could also enable model  
424 calibration using over distributions such as Zero-Inflation Poisson (ZIP) or integrating spatial  
425 autocorrelation for more robust inferences (Barnagaud et al., 2014; Guélat and Kéry, 2018; Martin et al.,  
426 2005).

427 Another drawback relies on the quantity of data collected through this structured CS scheme. Over  
428 the same breeding season, EPOC, a semi-structured scheme without temporal replicates nor fixed  
429 location requirements, collected three times the amount of complete checklists as EPOC-ODF scheme,  
430 highlighting CS trade-off of scheme standardisation upon data collection in space and time (Devictor et  
431 al., 2010). One way to address this trade-off is the use of data integration approaches mobilising multiple

432 data sources for ecological inferences (Zipkin et al., 2021, 2019) either by estimating abundance of less  
433 recorded species through traits associations (Callaghan et al., 2022, 2021; Robinson et al., 2022) or  
434 constructing joint likelihoods (Fithian et al., 2015; Fletcher et al., 2019).

435 As conservation policy decisions depend on uncertainty levels (Freckleton, 2020; Williams, 2003),  
436 assessing measurement error through integration of the detection process (Nichols et al., 2011) could  
437 provide more reliable ecological inferences (Guillera-Arroita et al., 2014). CS schemes are becoming more  
438 and more a reliable source of data to ensure biodiversity monitoring (Chandler et al., 2017) and can,  
439 through standardisation (Buckland and Johnston, 2017; Johnston et al., 2019), contribute to the  
440 calibration of data-hungry models such as hierarchical models for reliable ecological inferences (Isaac et  
441 al., 2020; Johnston et al., 2022; Kéry and Royle, 2021).

442

443

## Conclusion

444 Our results suggested an overall under-estimation in the population sizes of French common breeding  
445 birds estimated from the last French Breeding Bird atlas. Using large-scale datasets from citizen science  
446 obtained from standard scheme initiatives allowed inferring the variation in species abundance while  
447 explicitly modelling the detection process separately from the ecological one. Not accounting for the  
448 observation process might have resulted in misleading expert-only based estimations of population sizes  
449 in the previous atlas, at least for some widespread species not benefitting from exhaustive surveys. In  
450 conclusion, our results advocate for more reliance on the use of statistical tools accounting for the  
451 detection process, such as hierarchical models, which, in association with large-scale citizen science data,  
452 could constitute a standard methodology for inferring actual abundance from breeding bird atlases or  
453 biodiversity surveys deployed at national or geographically broader scales.

454

455

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470

471

## Conflict of interest disclosure

472 The authors declare that they comply with the PCI rule of having no financial conflicts of interest in  
473 relation to the content of the article

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## Data, scripts, code, and supplementary information availability

476 Data, scripts and code are available online: <https://doi.org/10.5281/zenodo.10696773> ; Nabias et al,  
477 2024

478 Supplementary information is available online: <https://doi.org/10.5281/zenodo.10696773> ; Nabias et  
479 al, 2024

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